#9
MW 3-8,01   1652

ENTERED

RAW SEQUENCE LISTING   DATE: 03/08/2001
PATENT APPLICATION: US/09/273,957 TIME: 13:29:26

Input Set : A:\GC477C1-SEQLIST.txt
Output Set: N:\CRF3\03082001\I273957.raw

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 3 <110> APPLICANT: Wang, Huaming
 4         Wang, Cynthia C.
 5         Amory, Antoine
 6         Dhaese, Patrick
 7         Lambrechts-Rongvaux, Annick
 9 <120> TITLE OF INVENTION: Novel Phenol Oxidizing Enzyme Enzymes
11 <130> FILE REFERENCE: GC477C1
13 <140> CURRENT APPLICATION NUMBER: US 09/273,957
14 <141> CURRENT FILING DATE: 1999-03-22
16 <160> NUMBER OF SEQ ID NOS: 14
18 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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21 <211> LENGTH: 1791
22 <212> TYPE: DNA
23 <213> ORGANISM: Stachybotrys chartarium
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28  actgaggtct tcgctgactc cctccttgct gcagcaggcg atgacgactg ggagtcacct     180
29  ccatacaact tgctttacag gaatgccctg ccaattccac ctgtcaagca gcccaagatg     240
30  atcattacca accctgtcac cggcaaggac atttggtact atgagatcga gatcaagcca     300
31  tttcagcaaa ggatttaccc caccttgcgc cctgccactc tcgtcggcta cgatggcatg     360
32  agccctggtc ctactttcaa tgttcccaga ggaacagaga ctgtagttag gttcatcaac     420
33  aatgccaccg tggagaactc ggtccatctg cacggctccc catcgcgtgc ccctttcgat     480
34  ggttgggctg aagatgtgac cttccctggc gagtacaagg attactactt tcccaactac     540
35  caatccgccc gccttctgtg gtaccatgac cacgctttca tgaagactac tgagaatgcc     600
36  tactttggtc aggctggcgc ctacattatc aacgacgagg ctgaggatgc tctcggtctt     660
37  cctagtggct atggcgagtt cgatatccct ctgatcctga cggccaagta ctataacgcc     720
38  gatggtaccc tgcgttcgac cgagggtgag gaccaggacc tgtggggaga tgtcatccat     780
39  gtcaacggac agccatggcc tttccttaac gtccagcccc gcaagtaccg tttccgattc     840
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41  gtcagaattc ctttccaagt cattgcctct gatgctggtc tccttcaagc ccccgttcag     960
42  acctctaacc tctaccttgc tgttgccgag cgttacgaga tcattattga cttcaccaac    1020
43  tttgctggcc agactcttga cctgcgcaac gttgctgaga ccaacgatgt cggcgacgag    1080
44  gatgagtacg ctcgcactct cgaggtgatg cgcttcgtcg tcagctctgg cactgttgag    1140
45  gacaacagcc aggtcccctc cactctccgt gacgttcctt tccctcctca caaggaaggc    1200
46  cccgccgaca agcacttcaa gtttgaacgc agcaacggac actacctgat caacgatgtt    1260
47  ggctttgccg atgtcaatga gcgtgtcctg gccaagcccg agctcggcac cgttgaggtc    1320
48  tgggagctcg agaactcctc tggaggctgg agccaccccg tccacattca ccttgttgac    1380
49  ttcaagatcc tcaagcgaac tggtggtcgt ggccaggtca tgccctacga gtctgctggt    1440
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51  ccctggactg gagcttacat gtggcactgt cacaacctca ttcacgagga taacgacatg    1560
52  atggctgtat tcaacgtcac cgccatggag gagaagggat atcttcagga ggacttcgag    1620
53  gacccccatga accccaagtg gcgcgccgtt ccttacaacc gcaacgactt ccatgctcgc    1680
54  gctggaaact tctccgccga gtccatcact gcccgagtgc aggagctggc cgagcaggag    1740
55  ccgtacaacc gcctcgatga gatcctggag gatcttggaa tcgaggagta a             1791
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66          20                  25                  30
67 Val Asp Pro Glu Val Lys Thr Glu Val Phe Ala Asp Ser Leu Leu Ala
68          35                  40                  45
69 Ala Ala Gly Asp Asp Asp Trp Glu Ser Pro Pro Tyr Asn Leu Leu Tyr
70      50                  55                  60
71 Arg Asn Ala Leu Pro Ile Pro Pro Val Lys Gln Pro Lys Met Ile Ile
72 65                  70                  75                  80
73 Thr Asn Pro Val Thr Gly Lys Asp Ile Trp Tyr Tyr Glu Ile Glu Ile
74              85                  90                  95
75 Lys Pro Phe Gln Gln Arg Ile Tyr Pro Thr Leu Arg Pro Ala Thr Leu
76              100                 105                 110
77 Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Asn Val Pro Arg
78          115                 120                 125
79 Gly Thr Glu Thr Val Val Arg Phe Ile Asn Asn Ala Thr Val Glu Asn
80      130                 135                 140
81 Ser Val His Leu His Gly Ser Pro Ser Arg Ala Pro Phe Asp Gly Trp
82 145              150                 155                 160
83 Ala Glu Asp Val Thr Phe Pro Gly Glu Tyr Lys Asp Tyr Tyr Phe Pro
84              165                 170                 175
85 Asn Tyr Gln Ser Ala Arg Leu Leu Trp Tyr His Asp His Ala Phe Met
86              180                 185                 190
87 Lys Thr Ala Glu Asn Ala Tyr Phe Gly Gln Ala Gly Ala Tyr Ile Ile
88          195                 200                 205
89 Asn Asp Glu Ala Glu Asp Ala Leu Gly Leu Pro Ser Gly Tyr Gly Glu
90      210                 215                 220
91 Phe Asp Ile Pro Leu Ile Leu Thr Ala Lys Tyr Tyr Asn Ala Asp Gly
92 225              230                 235                 240
93 Thr Leu Arg Ser Thr Glu Gly Glu Asp Gln Asp Leu Trp Gly Asp Val
94              245                 250                 255
95 Ile His Val Asn Gly Gln Pro Trp Pro Phe Leu Asn Val Gln Pro Arg
96              260                 265                 270
97 Lys Tyr Arg Phe Arg Phe Leu Asn Ala Ala Val Ser Arg Ala Trp Leu
98          275                 280                 285
99 Leu Tyr Leu Val Arg Thr Ser Ser Pro Asn Val Arg Ile Pro Phe Gln
100     290                 295                 300
101 Val Ile Ala Ser Asp Ala Gly Leu Leu Gln Ala Pro Val Gln Thr Ser
102 305             310                 315                 320
103 Asn Leu Tyr Leu Ala Val Ala Glu Arg Tyr Glu Ile Ile Ile Asp Phe
104              325                 330                 335
105 Thr Asn Phe Ala Gly Gln Thr Leu Asp Leu Arg Asn Val Ala Glu Thr
106              340                 345                 350
107 Asn Asp Val Gly Asp Glu Asp Glu Tyr Ala Arg Thr Leu Glu Val Met
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Input Set : A:\GC477C1-SEQLIST.txt
Output Set: N:\CRF3\03082001\I273957.raw

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109  Arg Phe Val Val Ser Ser Gly Thr Val Glu Asp Asn Ser Gln Val Pro
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111  Ser Thr Leu Arg Asp Val Pro Phe Pro Pro His Lys Glu Gly Pro Ala
112  385               390               395               400
113  Asp Lys His Phe Lys Phe Glu Arg Ser Asn Gly His Tyr Leu Ile Asn
114                405               410               415
115  Asp Val Gly Phe Ala Asp Val Asn Glu Arg Val Leu Ala Lys Pro Glu
116              420               425               430
117  Leu Gly Thr Val Glu Val Trp Glu Leu Glu Asn Ser Ser Gly Gly Trp
118          435               440               445
119  Ser His Pro Val His Ile His Leu Val Asp Phe Lys Ile Leu Lys Arg
120      450               455               460
121  Thr Gly Gly Arg Gly Gln Val Met Pro Tyr Glu Ser Ala Gly Leu Lys
122  465               470               475               480
123  Asp Val Val Trp Leu Gly Arg Gly Glu Thr Leu Thr Ile Glu Ala His
124              485               490               495
125  Tyr Gln Pro Trp Thr Gly Ala Tyr Met Trp His Cys His Asn Leu Ile
126          500               505               510
127  His Glu Asp Asn Asp Met Met Ala Val Phe Asn Val Thr Ala Met Glu
128      515               520               525
129  Glu Lys Gly Tyr Leu Gln Glu Asp Phe Glu Asp Pro Met Asn Pro Lys
130      530               535               540
131  Trp Arg Ala Val Pro Tyr Asn Arg Asn Asp Phe His Ala Arg Ala Gly
132  545               550               555               560
133  Asn Phe Ser Ala Glu Ser Ile Thr Ala Arg Val Gln Glu Leu Ala Glu
134              565               570               575
135  Gln Glu Pro Tyr Asn Arg Leu Asp Glu Ile Leu Glu Asp Leu Gly Ile
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137  Glu Glu
140  <210> SEQ ID NO: 3
141  <211> LENGTH: 3677
142  <212> TYPE: DNA
143  <213> ORGANISM: Stachybotrys chartarum
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148  ggggcacaga ctatcaagtg agacatatag gatgcatgtc tttcatagcc acagttaggg     180
149  tggtgaccta ctcgaagagg ccccgacttg catgcatacg acatgtcgct tccatgcaac     240
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151  cctttttgttt cttttccttt ctcaacgacg cgtgagcgtg gttaacttga gcaaggccga     360
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155  tctcttccgc atcaagcctc tatgcccgac gacaacacct cattggcccg gaccactttg     600
156  agcgcgcacg caccttcgcg ccgaaggagt tgataacacc cttcaccctt gcccaatgat     660
157  ggagttttgg tctatttgtc atgatcacct cacattcact agatcacgga tcctggaaga     720
158  gggtgtggaa gccagaccag cttgtccctg ttcttgcaga ctcaggtcag ctcctagcgg     780
159  ctatcacagc tcaggattat caagtcccgt aaagtccaga ccctttttcat tgtatgatgc     840
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161  gctgaagcat cgtgagatct ataaaggtct ccgaatcctc ggtgaagtca gaatcgtctc    960
162  tccacaccag tcaacaacaa gcttctttct cttacagctt agcctgagca cattcacaga   1020
163  actcttccct tcttttcgtc aatatgctgt tcaagtcatg gcaactggca gcagcctccg   1080
164  ggctcctgtc tggagtcctc ggcatcccga tggacaccgg cagccacccc attgaggctg   1140
165  ttgatcccga agtgaagact gaggtcttcg ctgactccct ccttgctgca gcaggcgatg   1200
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167  ttccctcgat aactaactct tatagaaatg ccctgccaat tccacctgtc aagcagccca   1320
168  agatgtatgt ctttgatttt ctacgaagca actcggcccc gactaatgta ttctaggatc   1380
169  attaccaacc ctgtcaccgg caaggacatt tggtactatg agatcgagat caagccattt   1440
170  cagcaaaggg tgagtttgct cagaaacctt gtggtaatta atcattgtta ctgacccttt   1500
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174  gaagatgtga ccttccctgg cgagtacaag gattactact ttcccaacta ccaatccgcc   1740
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176  ttggctacct ttggctaacc aacttccttt cgtagactgc tgagaatgcc tactttggtc   1860
177  aggctggcgc ctacattatc aacgacgagg ctgaggatgc tctcggtctt cctagtggct   1920
178  atggcgagtt cgatatccct ctgatcctga cggccaagta ctataacgcc gatggtaccc   1980
179  tgcgttcgac cgagggtgag gaccaggacc tgtgggagaga tgtcatccat gtcaacggac   2040
180  agccatggcc tttccttaac gtccagcccc gcaagtaccg tttccgattc ctcaacgctg   2100
181  ccgtgtctcg tgcttggctc ctctacctcg tcaggaccag ctctcccaac gtcagaattc   2160
182  ctttccaagt cattgcctct gatgctggtc tccttcaagc ccccgttcag acctctaacc   2220
183  tctaccttgc tgttgccgag cgttacgaga tcattattgg tatgccctcc cctctcacga   2280
184  atgagtcaag aactctaaga ctaacacttg tagacttcac caactttgct ggccagactc   2340
185  ttgacctgcg caacgttgct gagaccaacg atgtcggcga cgaggatgag tacgctcgca   2400
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187  cctccactct ccgtgacgtt cctttccctc ctcacaagga aggcccgcc gacaagcact   2520
188  tcaagtttga acgcagcaac ggacactacc tgatcaacga tgttggcttt gccgatgtca   2580
189  atgagcgtgt cctggccaag cccgagctcg gcaccgttga ggtctgggag ctcgagaact   2640
190  cctctggagg ctggagccac cccgtccaca ttcaccttgt tgacttcaag atcctcaagc   2700
191  gaactggtgg tcgtggccag gtcatgccct acgagtctgc tggtcttaag gatgtcgtct   2760
192  ggttgggcag gggtgagacc ctgaccatcg aggcccacta ccaaccctgg actggagctt   2820
193  acatgtggca ctgtcacaac ctcattcacg aggataacga catgatggct gtattcaacg   2880
194  tcaccgccat ggaggagaag ggatatcttc aggaggactt cgaggacccc atgaacccca   2940
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196  ccgagtccat cactgcccga gtgcaggagc tggccgagca ggagccgtac aaccgcctcg   3060
197  atgagatcct ggaggatctt ggaatcgagg agtaaacccc gagccacaag ctctacaatc   3120
198  gtttttgagtc ttaagacgag gctcttggtg cgtattcttt tcttccctac ggggaactcc   3180
199  gctgtccact gcgatgtgaa ggaccatcac aaagcaacgt atatattgga ctcaccactg   3240
200  tcattaccgc ccacttgtac ctattcgatt cttgttcaaa cttttctagt gcgagagtgt   3300
201  ccatagtcaa gaaacgccca tagggctatc gtctaaactg aactattgtg tggtctgtga   3360
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203  tacaggatca gtttctcatg agattacatc cgtctaatgt ttgtccatga gagtywagct   3480
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205  gacaagttag gtaagttgct tggtatccga aaatgactca ggctccctca ttaggttgca   3600
206  tgtgaaaacc ttcagcaact catgggtgtt gggaccaaat catccatacc tgattttgat   3660
207  aactgacctg ggtcaat                                                   3677
209  <210> SEQ ID NO: 4
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RAW SEQUENCE LISTING   DATE: 03/08/2001
PATENT APPLICATION: US/09/273,957   TIME: 13:29:26

Input Set : A:\GC477C1-SEQLIST.txt
Output Set: N:\CRF3\03082001\I273957.raw

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211 <212> TYPE: PRT
212 <213> ORGANISM: Myrothecium Verracaria
214 <400> SEQUENCE: 4
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218             20                  25                  30
219 Gly His Leu Phe Lys Arg Val Ala Gln Ile Ser Pro Gln Tyr Pro Met
220             35                  40                  45
221 Phe Thr Val Pro Leu Pro Ile Pro Pro Val Lys Gln Pro Arg Leu Thr
222     50                  55                  60
223 Val Thr Asn Pro Val Asn Gly Gln Glu Ile Trp Tyr Tyr Glu Val Glu
224 65                  70                  75                  80
225 Ile Lys Pro Phe Thr His Gln Val Tyr Pro Asp Leu Gly Ser Ala Asp
226                 85                  90                  95
227 Leu Val Gly Tyr Asp Gly Met Ser Pro Gly Pro Thr Phe Gln Val Pro
228             100                 105                 110
229 Arg Gly Val Glu Thr Val Val Arg Phe Ile Asn Asn Ala Glu Ala Pro
230             115                 120                 125
231 Asn Ser Val His Leu His Gly Ser Phe Ser Arg Ala Ala Phe Asp Gly
232     130                 135                 140
233 Trp Ala Glu Asp Ile Thr Glu Pro Gly Ser Phe Lys Asp Tyr Tyr Tyr
234 145                 150                 155                 160
235 Pro Asn Arg Gln Ser Ala Arg Thr Leu Trp Tyr His Asp His Ala Met
236             165                 170                 175
237 His Ile Thr Ala Glu Asn Ala Tyr Arg Gly Gln Ala Gly Leu Tyr Met
238             180                 185                 190
239 Leu Thr Asp Pro Ala Glu Asp Ala Leu Asn Leu Pro Ser Gly Tyr Gly
240             195                 200                 205
241 Glu Phe Asp Ile Pro Met Ile Leu Thr Ser Lys Gln Tyr Thr Ala Asn
242     210                 215                 220
243 Gly Asn Leu Val Thr Thr Asn Gly Glu Leu Asn Ser Phe Trp Gly Asp
244 225                 230                 235                 240
245 Val Ile His Val Asn Gly Gln Pro Trp Pro Phe Lys Asn Val Glu Pro
246             245                 250                 255
247 Arg Lys Tyr Arg Phe Arg Phe Leu Asp Ala Ala Val Ser Arg Ser Phe
248             260                 265                 270
249 Gly Leu Tyr Phe Ala Asp Thr Asp Ala Ile Asp Thr Arg Leu Pro Phe
250             275                 280                 285
251 Lys Val Ile Ala Ser Asp Ser Gly Leu Leu Glu His Pro Ala Asp Thr
252     290                 295                 300
253 Ser Leu Leu Tyr Ile Ser Met Ala Glu Arg Tyr Glu Val Val Phe Asp
254 305                 310                 315                 320
255 Phe Ser Asp Tyr Ala Gly Lys Thr Ile Glu Leu Arg Asn Leu Gly Gly
256             325                 330                 335
257 Ser Ile Gly Gly Ile Gly Thr Asp Thr Asp Tyr Asp Asn Thr Asp Lys
258             340                 345                 350
259 Val Met Arg Phe Val Val Ala Asp Asp Thr Thr Gln Pro Asp Thr Ser
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FYI

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 03/08/2001
PATENT APPLICATION: US/09/273,957 TIME: 13:29:27

Input Set : A:\GC477C1-SEQLIST.txt
Output Set: N:\CRF3\03082001\I273957.raw

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L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
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